

SEQUENCE LISTING

<110> Helix Research Institute

<120> NOVEL GENES ASSOCIATED WITH THE MAINTENANCE
OF DIFFERENTIATION OF SMOOTH MUSCLE CELLS

<130> H1-107PCT1

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<150> JP 1999-248036

<151> 1999-07-29

<150> JP 2000-118776

<151> 2000-01-11

<150> JP 2000-183767

<151> 2000-05-02

<150> US 60/159590

<151> 1999-10-18

<150> US 60/183322

<151> 2000-02-17

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<170> PatentIn Ver. 2.0

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<211> 2256

<212> DNA

<213> Homo sapiens

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<221> CDS

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agcc atg gca gcg ctg cgc tac gcg ggg ctg gac gac acg gac agt gag 169

Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu

1

5

10

15

gac gag ctg cct ccg ggc tgg gag gag aga acc acc aag gac ggc tgg 217

Asp Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp

20

25

30

gtt tac tac gcc aat cac acc gag gag aag act cag tgg gaa cat cca 265

Val Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro

35

40

45

aaa act gga aaa aga aaa cga gtg gca gga gat ttg cca tac gga tgg 313

Lys Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp

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55

60

gaa caa gaa act gat gag aac gga caa gtg ttt ttt gtt gac cat ata 361

Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile

65

70

75

aat aaa aga acc acc tac ttg gac cca aga ctg gcg ttt act gtg gat 409

Asn Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp

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85

90

95

gat aat ccg acc aag cca acc acc cgg caa aga tac gac ggc agc acc 457

Asp Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr

100

105

110

act gcc atg gaa att ctc cag ggc ccg gat ttc act ggc aaa gtg gtt 505

Thr Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val

115

120

125

gtg gtc act gga gct aat tca gga ata ggg ttc gaa acc gcc aag tct 553

Val Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser

130

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140

ttt gcc ctc cat ggt gca cat gtg atc ttg gcc tgc agg aac atg gca 601

Phe Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala

145

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155

agg gcg agt gaa gca gtg tca cgc att tta gaa gaa tgg cat aaa gcc 649

Arg Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala

160

165

170

175

aag gta gaa gca atg acc ctg gac ctc gct ctg ctc cgt agc gtg cag 697

Lys Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln

180

185

190

cat ttt gct gaa gca ttc aag gcc aag aat gtg cct ctt cat gtg ctt 745

His Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu

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gtg tgc aac gca gca act ttt gct cta ccc tgg agt ctc acc aaa gat 793

Val Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp

210

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220

ggc ctg gag acc acc ttt caa gtg aat cat ctg ggg cac ttc tac ctt 841

Gly Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu

225

230

235

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gtc cag ctc ctc cag gat gtt ttg tgc cgc tca gct cct gcc cgt gtc 889
 Val Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val
 240 245 250 255

att gtg gtc tcc tca gag tcc cat cga ttt aca gat att aac gac tcc 937
 Ile Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser
 260 265 270

ttg gga aaa ctg gac ttc agt cgc ctc tct cca aca aaa aac gac tat 985
 Leu Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr
 275 280 285

tgg gcg atg ctg gct tat aac agg tcc aag ctc tgc aac atc ctc ttc 1033
 Trp Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe
 290 295 300

tcc aac gag ctg cac cgt cgc ctc tcc cca cgc ggg gtc acg tcg aac 1081
 Ser Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn
 305 310 315

gca gtg cat cct gga aat atg atg tac tcc aac att cat cgc agc tgg 1129
 Ala Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp
 320 325 330 335

tgg gtg tac aca ctg ctg ttt acc ttg gcg agg cct ttc acc aag tcc 1177

Trp Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser

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atg caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa 1225

Met Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu

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ctg gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg 1273

Leu Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met

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ccc tca cca gaa gct cag agc gaa gag acg gcc cgg acc ctg tgg gcg 1321

Pro Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala

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ctc agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc 1366

Leu Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly

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cagtgaggat gacagtgaca cccagaggga gtagaatagc cagaactacc aggtggcaaa 1966

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<210> 2

<211> 414

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<213> Homo sapiens

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Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val

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Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys

35 40 45

Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu

50 55 60

Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn

65 70 75 80

Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp

85 90 95

Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr

100 105 110

Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val Val

115

120

125

Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe

130

135

140

Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg

145

150

155

160

Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys

165

170

175

Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His

180

185

190

Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val

195

200

205

Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly

210

215

220

Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val

225

230

235

240

Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile

245

250

255

10/19

Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu

260

265

270

Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp

275

280

285

Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser

290

295

300

Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala

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310

315

320

Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp

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Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met

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Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu

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360

365

Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro

370

375

380

Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu

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Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly

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<213> Gallus gallus

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gaa gaa aaa aca cag tgg gaa cat cca aaa tct ggg aag agg aaa cgt 95

Glu Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg

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gtt gca gga ggt ctg cca tat gga tgg gag cag gag act gat gaa aat 143

Val Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn

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gga cag gtc tat ttt gta gac cac ata aac aaa aga act acc tat ctg 191

Gly Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu

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gat cca aga ttg gcc ttt aca gtt gaa gat aat cca gca aag cca cct 239

Asp Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro

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act aga caa aaa

251

Thr Arg Gln Lys

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<210> 4

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<212> PRT

<213> Gallus gallus

<400> 4

Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu Glu

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Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg Val

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Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly

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Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp

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Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro Thr

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Arg Gln Lys

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<211> 30

<212> RNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially

Synthesized Sequence

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agcaucgagu cggccuuguu ggccuacugg

<210> 6

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<212> DNA

<213> Artificial Sequence

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<211> 21

<212> DNA

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<210> 8

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<213> Artificial Sequence

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<210> 10

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<210> 11

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<212> DNA

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<223> Description of Artificial Sequence:Artificially
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<210> 12

<211> 22

<212> DNA

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<210> 13

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<212> DNA

<213> Artificial Sequence

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<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
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<210> 15

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<212> DNA

<213> Artificial Sequence

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<210> 16

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<212> DNA

<213> Artificial Sequence

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